



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 08:53 AM GMT

PDB ID : 3GDP
Title : Hydroxynitrile lyase from almond, monoclinic crystal form
Authors : Dreveny, I.; Gruber, K.; Kratky, C.
Deposited on : 2009-02-24
Resolution : 1.57 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

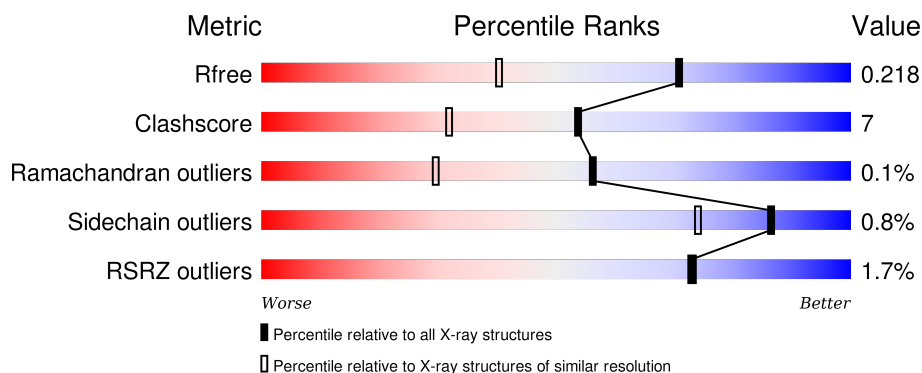
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.57 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	3815 (1.60-1.56)
Clashscore	102246	4131 (1.60-1.56)
Ramachandran outliers	100387	4021 (1.60-1.56)
Sidechain outliers	100360	4018 (1.60-1.56)
RSRZ outliers	91569	3823 (1.60-1.56)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	521	<div> <div>2%</div> <div>86%</div> <div>14%</div> </div>
1	B	521	<div> <div>2%</div> <div>88%</div> <div>12%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	IPA	A	522	-	-	-	X
2	IPA	B	522	-	-	-	X
4	NAG	A	524	-	-	-	X
6	NAG	A	530	-	-	-	X
9	NDG	B	533	-	-	-	X

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 10004 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

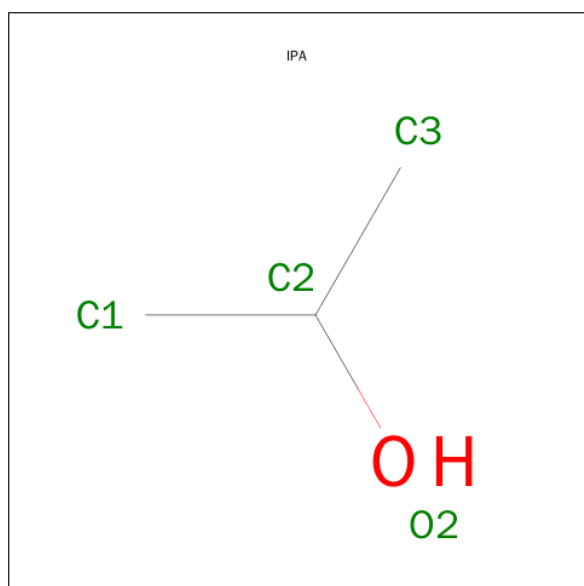
- Molecule 1 is a protein called R-oxynitrile lyase isoenzyme 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	521	Total	C	N	O	S	0	10	0
			4022	2556	669	789	8			
1	B	521	Total	C	N	O	S	0	8	0
			4015	2550	667	790	8			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	346	SER	ALA	SEE REMARK 999	UNP Q945K2
B	346	SER	ALA	SEE REMARK 999	UNP Q945K2

- Molecule 2 is ISOPROPYL ALCOHOL (three-letter code: IPA) (formula: C₃H₈O).



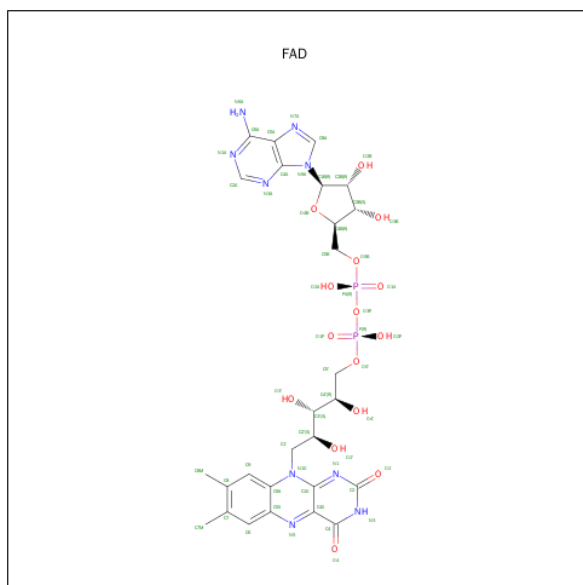
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	3	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			4	3	1		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 4 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is a polymer of unknown type called SUGAR (5-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	5	Total	C	N	O	0	0
			60	34	2	24		

- Molecule 6 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	3	Total	C	N	O	0	0
			38	22	2	14		

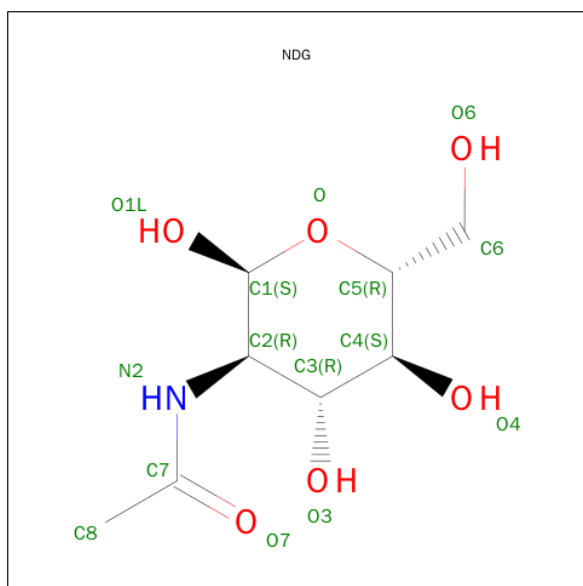
- Molecule 7 is a polymer of unknown type called SUGAR (5-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	5	Total	C	N	O	0	0
			60	34	2	24		

- Molecule 8 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	B	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 9 is SUGAR (2-(ACETYLAMINO)-2-DEOXY-A-D-GLUCOPYRANOSE) (three-letter code: NDG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	B	1	Total	C	N	O	0	0
			14	8	1	5		

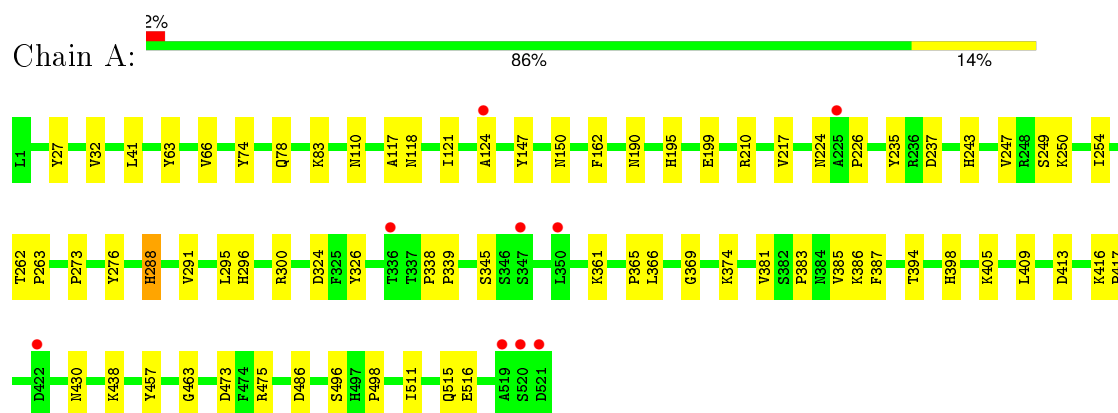
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	823	Total	O	0	0
			823	823		
10	B	766	Total	O	0	0
			766	766		

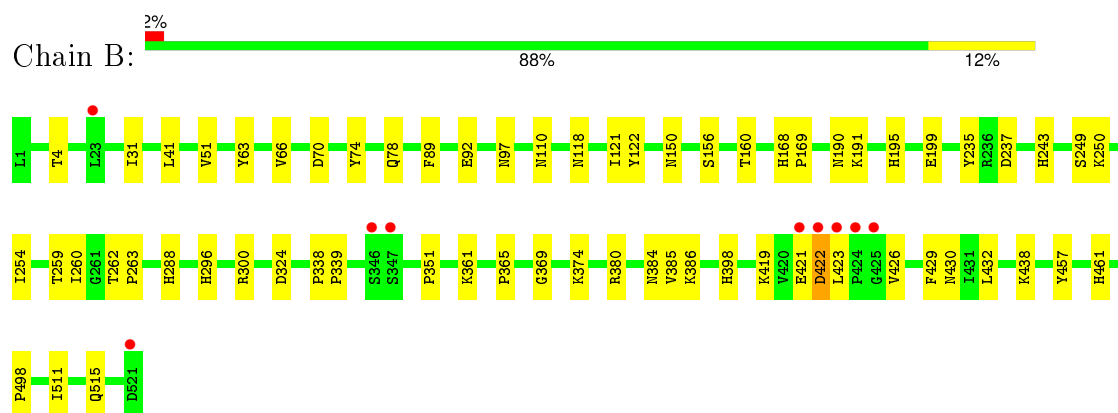
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($\text{RSRZ} > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: R-oxynitrile lyase isoenzyme 1



• Molecule 1: R-oxynitrile lyase isoenzyme 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	69.05Å 93.71Å 87.26Å 90.00° 106.39° 90.00°	Depositor
Resolution (Å)	38.25 – 1.57 38.25 – 1.57	Depositor EDS
% Data completeness (in resolution range)	95.6 (38.25-1.57) 95.7 (38.25-1.57)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.95 (at 1.57Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.186 , 0.210 0.193 , 0.218	Depositor DCC
R_{free} test set	14166 reflections (9.97%)	DCC
Wilson B-factor (Å ²)	11.7	Xtriage
Anisotropy	0.663	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 45.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 142084 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	10004	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 48.30 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 8.7740e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, NAG, NDG, IPA, FUC, FUL, FAD, MAN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.31	0/4181	0.63	0/5702
1	B	0.32	0/4161	0.63	0/5675
All	All	0.31	0/8342	0.63	0/11377

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4022	0	3882	61	0
1	B	4015	0	3874	45	0
2	A	4	0	8	1	0
2	B	4	0	8	0	0
3	A	53	0	31	2	0
3	B	53	0	31	1	0
4	A	28	0	26	0	0
4	B	14	0	13	0	0
5	A	60	0	52	1	0
6	A	38	0	34	0	0
7	B	60	0	52	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	B	50	0	43	0	0
9	B	14	0	13	0	0
10	A	823	0	0	9	0
10	B	766	0	0	5	0
All	All	10004	0	8067	108	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 108 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:295[B]:LEU:CD2	1:A:385[B]:VAL:CG2	2.03	1.35
1:A:475[B]:ARG:NH1	10:A:1007:HOH:O	1.60	1.31
1:A:295[B]:LEU:HD21	1:A:385[B]:VAL:HG21	1.19	1.19
1:A:295[B]:LEU:CD2	1:A:385[B]:VAL:HG23	1.75	1.06
1:A:295[B]:LEU:HD22	1:A:385[B]:VAL:HG23	1.42	1.01

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	529/521 (102%)	517 (98%)	11 (2%)	1 (0%)	52	27
1	B	527/521 (101%)	514 (98%)	13 (2%)	0	100	100
All	All	1056/1042 (101%)	1031 (98%)	24 (2%)	1 (0%)	56	29

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	486	ASP

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	453/443 (102%)	450 (99%)	3 (1%)	88	77
1	B	451/443 (102%)	447 (99%)	4 (1%)	84	69
All	All	904/886 (102%)	897 (99%)	7 (1%)	86	74

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	288	HIS
1	B	498	PRO
1	B	422	ASP
1	A	430	ASN
1	B	430	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	150	ASN
1	B	190	ASN
1	B	323	ASN
1	B	65	ASN
1	B	281	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

17 carbohydrates are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	NAG	A	525	1,5	14,14,15	0.59	0	15,19,21	0.76	1 (6%)
5	NAG	A	526	5	14,14,15	0.77	0	15,19,21	0.88	0
5	FUL	A	527	5	10,10,11	0.43	0	14,14,16	0.53	0
5	MAN	A	528	5	11,11,12	0.66	0	14,15,17	0.89	1 (7%)
5	MAN	A	529	5	11,11,12	0.55	0	14,15,17	0.55	0
6	NAG	A	530	1,6	14,14,15	0.55	0	15,19,21	0.80	1 (6%)
6	NAG	A	531	6	14,14,15	0.51	0	15,19,21	0.74	1 (6%)
6	FUC	A	532	6	10,10,11	0.48	0	14,14,16	0.52	0
7	NAG	B	524	7	14,14,15	0.47	0	15,19,21	0.66	1 (6%)
7	NAG	B	525	1,7	14,14,15	0.52	0	15,19,21	0.66	1 (6%)
7	FUC	B	526	7	10,10,11	0.47	0	14,14,16	0.53	0
7	BMA	B	527	7	11,11,12	0.41	0	14,15,17	0.34	0
7	MAN	B	528	7	11,11,12	0.47	0	14,15,17	0.61	0
8	NAG	B	529	1,8	14,14,15	0.57	0	15,19,21	1.12	2 (13%)
8	NAG	B	530	8	14,14,15	0.56	0	15,19,21	0.69	1 (6%)
8	BMA	B	531	8	11,11,12	0.45	0	14,15,17	0.52	0
8	MAN	B	532	8	11,11,12	0.51	0	14,15,17	0.58	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	A	525	1,5	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	A	526	5	-	0/6/23/26	0/1/1/1
5	FUL	A	527	5	-	0/0/17/20	0/1/1/1
5	MAN	A	528	5	-	0/2/19/22	0/1/1/1
5	MAN	A	529	5	-	0/2/19/22	0/1/1/1
6	NAG	A	530	1,6	-	0/6/23/26	0/1/1/1
6	NAG	A	531	6	-	0/6/23/26	0/1/1/1
6	FUC	A	532	6	-	0/0/17/20	0/1/1/1
7	NAG	B	524	7	-	0/6/23/26	0/1/1/1
7	NAG	B	525	1,7	-	0/6/23/26	0/1/1/1
7	FUC	B	526	7	-	0/0/17/20	0/1/1/1
7	BMA	B	527	7	-	0/2/19/22	0/1/1/1
7	MAN	B	528	7	-	0/2/19/22	0/1/1/1
8	NAG	B	529	1,8	-	0/6/23/26	0/1/1/1
8	NAG	B	530	8	-	0/6/23/26	0/1/1/1
8	BMA	B	531	8	-	0/2/19/22	0/1/1/1
8	MAN	B	532	8	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	B	529	NAG	C2-N2-C7	-2.55	119.76	123.04
6	A	530	NAG	C2-N2-C7	-2.44	119.90	123.04
6	A	531	NAG	C2-N2-C7	-2.29	120.10	123.04
8	B	529	NAG	C4-C3-C2	-2.24	107.74	111.23
5	A	525	NAG	C2-N2-C7	-2.06	120.39	123.04

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	526	NAG	1	0
5	A	527	FUL	1	0
7	B	524	NAG	1	0
7	B	526	FUC	1	0

5.6 Ligand geometry

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	IPA	A	522	-	3,3,3	0.52	0	3,3,3	0.83	0
3	FAD	A	523	-	48,58,58	2.09	16 (33%)	54,89,89	1.87	12 (22%)
4	NAG	A	524	1	14,14,15	0.50	0	15,19,21	0.60	0
4	NAG	A	533	1	14,14,15	0.58	0	15,19,21	0.79	1 (6%)
2	IPA	B	522	-	3,3,3	0.51	0	3,3,3	0.84	0
3	FAD	B	523	-	48,58,58	2.11	16 (33%)	54,89,89	1.89	12 (22%)
9	NDG	B	533	-	14,14,15	0.52	0	15,19,21	0.79	1 (6%)
4	NAG	B	534	1	14,14,15	0.55	0	15,19,21	0.65	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	IPA	A	522	-	-	0/0/0/0	0/0/0/0
3	FAD	A	523	-	-	0/30/50/50	0/6/6/6
4	NAG	A	524	1	-	0/6/23/26	0/1/1/1
4	NAG	A	533	1	-	0/6/23/26	0/1/1/1
2	IPA	B	522	-	-	0/0/0/0	0/0/0/0
3	FAD	B	523	-	-	0/30/50/50	0/6/6/6
9	NDG	B	533	-	-	0/6/23/26	0/1/1/1
4	NAG	B	534	1	-	0/6/23/26	0/1/1/1

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	523	FAD	PA-O2A	-4.14	1.37	1.54
3	A	523	FAD	PA-O2A	-4.08	1.37	1.54
3	B	523	FAD	P-O2P	-3.50	1.40	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	523	FAD	P-O2P	-3.37	1.40	1.54
3	A	523	FAD	C10-N10	-2.44	1.36	1.39

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	523	FAD	C4X-C4-N3	-4.82	117.00	123.59
3	B	523	FAD	C4X-C4-N3	-4.70	117.16	123.59
3	A	523	FAD	C4-C4X-C10	-4.09	117.32	119.94
3	B	523	FAD	C4-C4X-C10	-4.05	117.35	119.94
3	B	523	FAD	N3A-C2A-N1A	-3.96	125.86	128.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	522	IPA	1	0
3	A	523	FAD	2	0
3	B	523	FAD	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	521/521 (100%)	-0.14	9 (1%) 73 73	6, 11, 21, 36	2 (0%)
1	B	521/521 (100%)	-0.06	9 (1%) 73 73	7, 12, 24, 40	3 (0%)
All	All	1042/1042 (100%)	-0.10	18 (1%) 73 73	6, 11, 23, 40	5 (0%)

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	422	ASP	3.4
1	A	124	ALA	3.1
1	A	422[A]	ASP	3.0
1	B	425	GLY	2.8
1	B	423	LEU	2.7

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
6	NAG	A	530	14/15	0.87	0.14	4.29	24,29,35,36	0
5	NAG	A	525	14/15	0.86	0.12	1.48	14,20,25,29	0
8	NAG	B	529	14/15	0.88	0.11	1.41	14,19,22,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
7	MAN	B	528	11/12	0.62	0.29	1.20	43,45,46,46	0
7	NAG	B	525	14/15	0.91	0.12	-	18,22,25,27	0
5	MAN	A	528	11/12	0.55	0.31	-	46,48,50,52	0
6	FUC	A	532	10/11	0.74	0.31	-	39,41,42,43	0
5	FUL	A	527	10/11	0.59	0.45	-	35,39,41,41	0
8	BMA	B	531	11/12	0.61	0.22	-	42,44,47,49	0
5	NAG	A	526	14/15	0.60	0.22	-	30,33,39,43	0
8	MAN	B	532	11/12	0.58	0.28	-	50,50,52,52	0
6	NAG	A	531	14/15	0.76	0.31	-	40,42,43,44	0
8	NAG	B	530	14/15	0.77	0.16	-	27,30,35,38	0
7	FUC	B	526	10/11	0.89	0.28	-	31,34,35,36	0
5	MAN	A	529	11/12	0.59	0.26	-	52,52,53,53	0
7	NAG	B	524	14/15	0.86	0.22	-	28,30,35,36	0
7	BMA	B	527	11/12	0.76	0.26	-	38,40,41,42	0

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
9	NDG	B	533	14/15	0.55	0.28	5.97	40,43,45,45	0
2	IPA	A	522	4/4	0.92	0.10	2.86	19,20,20,21	0
4	NAG	A	524	14/15	0.90	0.14	2.49	15,17,21,22	0
2	IPA	B	522	4/4	0.93	0.10	2.00	19,20,21,21	0
4	NAG	B	534	14/15	0.86	0.11	1.32	15,21,24,26	0
3	FAD	B	523	53/53	0.98	0.07	-0.36	5,7,8,9	0
3	FAD	A	523	53/53	0.98	0.07	-0.37	4,6,9,9	0
4	NAG	A	533	14/15	0.58	0.29	-	37,41,42,43	0

6.5 Other polymers

There are no such residues in this entry.